

Serial No. 09/766,399  
Group Art Unit: 1634

AMENDMENTS

In the Claims

Please cancel claims 1, 17 and 18 without prejudice. Please amend Claims 2, 7, 8, 12 and 16 as follows:

2. (Amended) An isolated plant promoter comprising at least one synthetic multimeric promoter element region that is capable of driving transcription in a plant cell, wherein said promoter comprises a polynucleotide selected from the group consisting of:

A<sup>1</sup> (a) a nucleotide sequence comprising promoter elements GT-2 comprising SEQ ID NO.:24, ABRE1 comprising SEQ ID NO.: 2, ABRE1 comprising SEQ ID NO.: 2, GT-2 comprising SEQ ID NO.:24, As-1 comprising SEQ ID NO.: 7, GT-2 comprising SEQ ID NO.:24, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.: 59, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.: 59, DRE1 comprising SEQ ID NO.: 59, As-1 comprising SEQ ID NO.: 7, DRE1 comprising SEQ ID NO.: 59, DRE1 comprising SEQ ID NO.: 59, and ABRE1 comprising SEQ ID NO.: 2, sequentially;

(b) a nucleotide sequence comprising SEQ ID NO.: 65;

(c) a nucleotide sequence of not less than 50 nucleotides that hybridizes under stringent conditions to a nucleotide sequence of (a) or (b), wherein said stringent conditions include hybridization in 50% formamide, 1M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60-65°C; and

(d) a polynucleotide which has at least about 90% sequence identity as determined by the GAP algorithm under default parameters across the full length of a sequence of (a) or (b).

A<sup>2</sup> 7. (Amended) A plant, or its parts, having stably incorporated into its genome a DNA construct comprising a plant promoter of claim 2 operably linked to a coding sequence.

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8. (Amended) A plant, or its parts, having stably incorporated into its genome a DNA construct comprising a plant promoter operably linked to a coding sequences, said plant promoter comprising at least one synthetic multimeric promoter element region that is capable of driving transcription in a plant cell, wherein said promoter comprises a polynucleotide selected from the group consisting of:

(a) a nucleotide sequence comprising promoter elements GT-2 comprising SEQ ID NO.:24, ABRE1 comprising SEQ ID NO.: 2, ABRE1 comprising SEQ ID NO.: 2, GT-2 comprising SEQ ID NO.:24, As-1 comprising SEQ ID NO.: 7, GT-2 comprising SEQ ID NO.:24, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.: 59, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.: 59, DRE1 comprising SEQ ID NO.: 59, As-1 comprising SEQ ID NO.: 7, DRE1 comprising SEQ ID NO.: 59, DRE1 comprising SEQ ID NO.: 59, and ABRE1 comprising SEQ ID NO.: 2, sequentially;

(b) a nucleotide sequence comprising SEQ ID NO.: 65;

(c) a nucleotide sequence of not less than 50 nucleotides that hybridizes under stringent conditions to a nucleotide sequence of (a) or (b), wherein said stringent conditions include hybridization in 50% formamide, 1M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60-65°C; and

(d) a polynucleotide which has at least about 90% sequence identity as determined by the GAP algorithm under default parameters across the full length of a sequence of (a) or (b).

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12. (Amended) A plant cell having stably incorporated into its genome a DNA construct comprising a plant promoter operably linked to a coding sequence, said plant promoter comprising at least one synthetic multimeric promoter element region that is capable of driving transcription in a plant cell, wherein said promoter comprises a polynucleotide selected from the group consisting of:

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Cont.

(a) a nucleotide sequence comprising promoter elements GT-2 comprising SEQ ID NO.:24, ABRE1 comprising SEQ ID NO.: 2, ABRE1 comprising SEQ ID NO.: 2, GT-2 comprising SEQ ID NO.:24, As-1 comprising SEQ ID NO.: 7, GT-2 comprising SEQ ID NO.:24, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.: 59, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.: 59, DRE1 comprising SEQ ID NO.: 59, As-1 comprising SEQ ID NO.: 7, DRE1 comprising SEQ ID NO.: 59, DRE1 comprising SEQ ID NO.: 59, and ABRE1 comprising SEQ ID NO.: 2, sequentially;

(b) a nucleotide sequence comprising SEQ ID NO.: 65;

(c) a nucleotide sequence of not less than 50 nucleotides that hybridizes under stringent conditions to the nucleotide sequence of (a) or (b), wherein said stringent conditions include hybridization in 50% formamide, 1M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60-65°C; and

(d) a polynucleotide which has at least about 90% sequence identity as determined by the GAP algorithm under default parameters across the full length of a sequence of (a) or (b).

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16. (Amended) A method for constitutively expressing a heterologous nucleotide sequence in a plant, said method comprising:

- (a) transforming a plant cell with a transformation vector comprising an expression cassette, said expression cassette comprising a plant promoter of claim 2 operably linked to a coding sequence; and
- (b) regenerating a stably transformed plant from said transformed cell, said plant having stably incorporated into its genome said expression cassette.